SEQUENCE LISTING

<110> Abbott Laboratories
      Mukerji, Pradip
      Huang, Yung-Sheng
      Das, Tapas
      Thurmond, Jennifer M.
      Pereira, Suzette L.

<120> DESATURASE GENES AND USES THEREOF

<130> 6763.US.P1

<140> Not Yet Assigned
<141> 2002-01-22

<150> US 09/769,863
<151> 2001-01-25

<160> 55

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO834

<221> misc_feature
<222> (3)...(3)
<223> b = g or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (9)...(9)
<223> y = t/u or c at position 9

<221> misc_feature
<222> (12)...(12)
<223> b = g or c or t/u at position 12

<221> misc_difference
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (24)...(24)
<223> b = g or c or t/u at position 24

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<221> misc_feature
<222> (30)...(30)
<223> b = g or c or t/u at position 30

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> y = t/u or c at position 36

<221> misc_feature
<222> (39)...(39)
<223> h = a or c or t/u at position 39

<221> misc_feature
<222> (42)...(42)
<223> h = a or c or t/u at position 42

<400> 1
gtbtaygayg tbaccgartg ggtbaagcgy cayccbgghg gh                    42

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO835

<221> misc_feature
<222> (3)...(3)
<223> h = a or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (33)...(33)
<223> y = tu or c at position 33

<221> misc_feature
<222> (39)...(39)
<223> b = g or c or t/u at position 39

<221> misc_feature
<222> (41)...(41)
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<223> y = t/u or c at position 41

<221> misc_feature
<222> (45)...(45)
<223> y = t/u or c at position 45

<400> 2
gghgcytccg cyaactggtg gaagcaycag cayaacgtbc aycay   45

<210> 3
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO836

<221> misc_feature
<222> (1)...(1)
<223> r = g or a at position 1

<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (7)...(7)
<223> v = a or g or c at position 7

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> d = a or g or t/u at position 43

<400> 3
rtgrtgvacg ttrtgctgrt gcttccacca gttrgcggar gcdcc   45

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

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<220>
<223> Reverse Primer RO838

<221> misc_feature
<222> (6)...(6)
<223> r = g or a at position 6

<221> misc_feature
<222> (12)...(12)
<223> r = g or a at position 12

<221> misc_feature
<222> (15)...(15)
<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (21)...(21)
<223> r = g or a at position 21

<221> misc_feature
<222> (24)...(24)
<223> s = g or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> r = g or a at position 27

<221> misc_feature
<222> (30)...(30)
<223> v = a or g or c at position 30

<400> 4
ttgatrgtct arctygtrgt rgasaarggv tggtac                        36

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO753

<221> misc_feature
<222> (10)...(10)
<223> n = a or g or c or t/u, unknown, or other at
      position 10

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (16)...(16)
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<223> n = a or g or c or t/u, unknown, or other at
      position 16

<221> misc_feature
<222> (18)...(19)
<223> r = g or a at positions 18-19

<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22

<400> 5
catcatcatn ggraanarrt grtg   24

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO754

<221> misc_feature
<222> (15)...(15)
<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> y = t/u or c at position 19

<221> misc_feature
<222> (21)...(21)
<223> n = a or g or c or t/u, unknown, or other at
      position 21

<221> misc_feature
<222> (24)...(24)
<223> y = t/u or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> n = a or g or c or t/u, unknown, or other at
      position 27

<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<400> 6
ctactactac tacaycayac ntayacnaay   30

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer RO923

<400> 7
cggtgcagtg gtggaagaac aagcacaac   29

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO899

<400> 8
agcggataac aatttcacac aggaaacagc   30

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO939

<400> 9
cgtagtactg ctcgaggagc ttgagcgccg   30

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO898

<400> 10
cccagtcacg acgttgtaaa acgacggcca g   31

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO951

<400> 11
tcaacagaat tcatggtcca ggggcaaaag gccgagaaga tctcg   45

<210> 12
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO960

<400> 12
atacgtaagc ttttacatgg cgggaaactc cttgaagaac tcgatcg   47

<210> 13
<211> 1362
<212> DNA
<213> Saprolegnia diclina

<400> 13
atggtccagg ggcaaaaggc cgagaagatc tcgtgggcga ccatccgtga gcacaaccgc 60
caagacaacg cgtggatcgt gatccaccac aaggtgtacg acatctcggc ctttgaggac 120
cacccgggcg gcgtcgtcat gttcacgcag gccggcgaag acgcgaccga tgcgttcgct 180
gtcttccacc cgagctcggc gctcaagctc ctcgagcagt actacgtcgg cgacgtcgac 240
cagtcgacgg cggccgtcga cacgtcgatc tcggacgagg tcaagaagag ccagtcggac 300
ttcattgcgt cgtaccgcaa gctgcgcctt gaagtcaagc gcctcggctt gtacgactcg 360
agcaagctct actacctcta caagtgcgcc tcgacgctga gcattgcgct tgtgtcggcg 420
gccatttgcc tccactttga ctcgacggcc atgtacatgg tcgcggctgt catccttggc 480
ctcttttacc agcagtgcgg ctggctcgcc atgactttc tgcaccacca agtgtttgag 540
aaccacttgt ttggcgacct cgtcggcgtc atggtcggca acctctggca gggcttctcg 600
gtgcagtggt ggaagaacaa gcacaacacg caccatgcga tccccaacct ccacgcgacg 660
cccgagatcg ccttccacgg cgacccggac attgacacga tgccgattct cgcgtggtcg 720
ctcaagatgg cgcagcacgc ggtcgactcg cccgtcgggc tcttcttcat gcgctaccaa 780
gcgtacctgt actttcccat cttgctcttt gcgcgtatct cgtgggtgat ccagtcggcc 840
atgtacgcct tctacaacgt tgggcccggc ggcacctttg acaaggtcca gtacccgctg 900
ctcgagcgcg ccggcctcct cctctactac ggctggaacc tcggccttgt gtacgcagcc 960
aacatgtcgc tgctccaagc ggctgcgttc ctctttgtga gccaggcgtc gtgcggcctc 1020
ttcctcgcga tggtctttag cgtcggccac aacggcatgg aggtctttga caaggacagc 1080
aagcccgatt ttttggaagct gcaagtgctc tcgacgcgca acgtgacgtc gtcgctctgg 1140
atcgactggt tcatgggcgg cctcaactac cagatcgacc accacttgtt cccgatggtg 1200
ccccggcaca acctccccggc gctcaacgtg ctcgtcaagt cgctctgcaa gcagtacgac 1260
atcccatacc acgagacggg cttcatcgcg ggcatggccg aggtcgtcgt gcacctcgag 1320
cgcatctcga tcgagttctt caaggagttt cccgccatgt aa   1362

<210> 14
<211> 453
<212> PRT
<213> Saprolegnia diclina

<400> 14
Met Val Gln Gly Gln Lys Ala Glu Lys Ile Ser Trp Ala Thr Ile Arg
1   5   10   15
Glu His Asn Arg Gln Asp Asn Ala Trp Ile Val Ile His His Lys Val
                20   25   30
Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe
            35   40   45
Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro
        50   55   60
Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp
65   70   75   80
Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys
                85   90   95
Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
            100   105   110
Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys
        115   120   125
Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu
        130   135   140

```
His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly
145                 150             155                 160
Leu Phe Tyr Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His His
            165             170                 175
Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val
            180             185                 190
Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His
            195             200                 205
Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala
    210             215             220
Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser
225             230             235                 240
Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe
            245             250             255
Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg
            260             265             270
Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly
            275             280             285
Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala
            290             295             300
Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala
305             310             315                 320
Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala
            325             330             335
Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly
            340             345             350
Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln
            355             360             365
Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe
            370             375             380
Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val
385             390             395                 400
Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys
            405             410             415
Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met
            420             425             430
Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys
            435             440             445
Glu Phe Pro Ala Met
    450
```

```
<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO851

<400> 15
ccatcaagac gtaccttgcg atc                                    23

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence
```

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<220>
<223> Primer RO941

<400> 16
gctgaacggg tggtacgagt cgaacgtg                                          28


<210> 17
<211> 42
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer RO953

<400> 17
acgagagaat tcatggcccc gcagacggag ctccgccagc gc                         42


<210> 18
<211> 46
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer RO956

<400> 18
aaaagactcg agttagccca tgtggatcgt ggcggcgatg ccctgc                     46


<210> 19
<211> 1413
<212> DNA
<213> Saprolegnia diclina

<400> 19
atggccccgc agacggagct ccgccagcgc cacgccgccg tcgccgagac gccggtggcc   60
ggcaagaagg cctttacatg gcaggaggtc gcgcagcaca acacggcggc ctcggcctgg   120
atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc   180
cgcgagatgg tgctgctgca cgccggtcgc gaggccaccg acacgttcga ctcgtaccac   240
ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agattggcac gttcacgggc   300
ccgtccgagt ttccgacctt caagccggac acgggcttct acaaggagtg ccgcaagcgc   360
gttggcgagt acttcaagaa gaacaacctc catccgcagg acggcttccc gggcctctgg   420
cgcatgatgg tcgtgtttgc ggtcgccggc ctcgccttgt acggcatgca cttttcgact   480
atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgctg   540
ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatgccgtt cttccattac   600
gtcgtcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac   660
cagcacgtcg tgggccacca catctacacg aacgtcgcgg gctcggaccc ggatcttccg   720
gtcaacatgg acggcgacat ccgccgcatc gtgaaccgcc aggtgttcca gcccatgtac   780
gcattccagc acatctacct tccgccgctc tatggcgtgc ttggcctcaa gttccgcatc   840
caggacttca ccgacacgtt cggctcgcac acgaacggcc cgatccgcgt caacccgcac   900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg   960
taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttcctc   1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc   1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc   1140
tcgcaggtca agacgtcggt cgactacgcc catggctcgt ggatgacgac gttccttgcc   1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac   1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc   1320
```

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ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catgggccag 1380
cagggcatcg ccgccacgat ccacatgggc taa                                  1413
```

<210> 20
<211> 470
<212> PRT
<213> Saprolegnia diclina

<400> 20

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Met Ala Pro Gln Thr Glu Leu Arg Gln Arg His Ala Ala Val Ala Glu
 1               5                  10                  15
Thr Pro Val Ala Gly Lys Lys Ala Phe Thr Trp Gln Glu Val Ala Gln
            20                  25                  30
His Asn Thr Ala Ala Ser Ala Trp Ile Ile Ile Arg Gly Lys Val Tyr
        35                  40                  45
Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val
        50                  55                  60
Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His
65                  70                  75                  80
Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly
                85                  90                  95
Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly
            100                 105                 110
Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn
        115                 120                 125
Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val
        130                 135                 140
Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr
145                 150                 155                 160
Ile Phe Ala Leu Gln Leu Ala Ala Ala Ala Leu Phe Gly Val Cys Gln
                165                 170                 175
Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr
            180                 185                 190
Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp
            195                 200                 205
Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val
        210                 215                 220
Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro
225                 230                 235                 240
Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe
            245                 250                 255
Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly
            260                 265                 270
Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly
            275                 280                 285
Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr
        290                 295                 300
Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val
305                 310                 315                 320
Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala
            325                 330                 335
Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn
            340                 345                 350
Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp
        355                 360                 365
Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys
        370                 375                 380
```

```
Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met Thr Thr Phe Leu Ala
385                 390                 395                 400
Gly Ala Leu Asn Tyr Gln Val Val His His Leu Phe Pro Ser Val Ser
                405                 410                 415
Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys
            420                 425                 430
Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe
            435                 440                 445
Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala
    450                 455                 460
Ala Thr Ile His Met Gly
465                 470
```

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<210> 21
<211> 914
<212> DNA
<213> Homo sapiens

<400> 21
atggaacatt ttgatgcatc acttagtacc tatttcaagg cattgctagg ccctcgagat 60
actagagtaa aaggatggtt tcttctggac aattatatac ccacatttat ctgctctgtc 120
atatatttac taattgtatg gctgggacca aaatacatga ggaataaaca gccattctct 180
tgccggggga ttttagtggt gtataacctt ggactcacac tgctgtctct gtatatgttc 240
tgtgagttag taacaggagt atgggaaggc aaatacaact tcttctgtca gggcacacgc 300
accgcaggag aatcagatat gaagattatc cgtgtcctct ggtggtacta cttctccaaa 360
ctcatagaat ttatggacac tttcttcttc atcctgcgca agaacaacca ccagatcacg 420
gtcctgcacg tctaccacca tgcctcgatg ctgaacatct ggtggtttgt gatgaactgg 480
gtcccctgcg ccactctta ttttggtgcc acacttaata gcttcatcca cgtcctcatg 540
tactcttact atggtttgtc gtcagtccct tccatgcgtc catacctctg gtggaagaag 600
tacatcactc aggggcagct gcttcagttt gtgctgacaa tcatccagac cagctgcggg 660
gtcatctggc cgtgcacatt ccctcttggt tggttgtatt ccagattgg atacattatt 720
tccctgattg ctctcttcac aaacttctac attcagacct acaacaagaa aggggcctcc 780
cgaaggaaag accacctgaa ggaccaccag aatgggtccg tggctgctgt gaatggacac 840
accaacagct tttcacccct ggaaaacaat gtgaagccaa ggaagctgcg gaaggattga 900
agtcaaagaa ttga 914
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```
<210> 22
<211> 957
<212> DNA
<213> Mortierella alpina

<400> 22
atggagtcga ttgcgccatt cctcccatca aagatgccgc aagatctgtt tatggacctt 60
gccaccgcta tcggtgtccg ggccgcgccc tatgtcgatc ctctcgaggc cgcgctggtg 120
gcccaggccg agaagtacat ccccacgatt gtccatcaca cgcgtgggtt cctggtcgcg 180
gtggagtcgc ctttggcccg tgagctgccg ttgatgaacc cgttccacgt gctgttgatc 240
gtgctcgctt atttggtcac ggtctttgtg ggcatgcaga tcatgaagaa ctttgagcgg 300
ttcgaggtca agacgttttc gctcctgcac aacttttgtc tggtctcgat cagcgcctac 360
atgtgcggtg ggatcctgta cgaggcttat caggccaact atggactgtt tgagaacgct 420
gctgatcata ccttcaaggg tcttcctatg ccaagatga tctggctctt ctacttctcc 480
aagatcatgg agtttgtcga caccatgatc atggtcctca gaagaacaa ccgccagatc 540
tccttcttgc acgtttacca ccacagctcc atcttcacca tctggtggtt ggtcaccttt 600
gttgcaccca cggtgaagc ctacttctct gctgcgttga actcgttcat ccatgtgatc 660
atgtacggct actacttctt gtcggccttg gcttcaagc aggtgtcgtt catcaagttc 720
tacatcacgc gctcgcagat gacacagttc tgcatgatgt cggtccagtc ttcctgggac 780
atgtacgcca tgaaggtcct tggccgcccc ggataccct tcttcatcac ggctctgctt 840
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tggttctaca tgtggaccat gctcggtctc ttctacaact tttacagaaa gaacgccaag 900
ttggccaagc aggccaaggc cgacgctgcc aaggagaagg caaggaagtt gcagtaa    957
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<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO936

<400> 23
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gtcgggcaag gcggaaaagt acctcaagag                                  30
```

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO937

<400> 24
```
aaacctgtag acaatgtgga ggggcgtggg                                  30
```

<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO972

<400> 25
```
atacttgaat tcatgggacg cggcggcgaa ggtcaggtga ac                    42
```

<210> 26
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO949

<400> 26
```
cttatactcg agctaagcgg ccttggccgc cgcctggcc                        39
```

<210> 27
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO950

<400> 27
```
cttatactcg agtaaatggc tcgcgaggcg aagcgagtgg c                     41
```

<210> 28
<211> 1320
<212> DNA
<213> Thraustochytrium aureum

<400> 28
atgggacgcg gcggcgaagg tcaggtgaac agcgcgcagg tggcacaagg cggtgcggga 60
acgcgaaaga cgatcctgat cgagggcgag gtctacgatg tcaccaactt taggcacccc 120
ggcgggtcga tcatcaagtt tctcacgacc gacggcaccg aggctgtgga cgcgacgaac 180
gcgtttcgcg agtttcactg ccggtcgggc aaggcggaaa agtacctcaa gagcctgccc 240
aagctcggcg cgccgagcaa gatgaagttt gacgccaagg agcaggcccg cgcgacgcg 300
atcacgcgag actacgtcaa gctgcgcgag gagatggtgg ccgagggcct cttcaagccc 360
gcgcccctcc acattgtcta caggtttgcg gagatcgcag ccctgttcgc ggcctcgttc 420
tacctgtttt cgatgcgcgg aaacgtgttc gccacgctcg cggccatcgc agtcgggggc 480
atcgcgcagg gccgctgcgg ctggctcatg cacgagtgcg gacacttctc gatgaccggg 540
tacatcccgc ttgacgtgcg cctgcaggag ctggtgtacg gcgtggggtg ctcgatgtcg 600
gcgagctggt ggcgcgttca gcacaacaag caccacgcga ccccgcagaa actcaagcac 660
gacgtcgacc tcgacaccct gccgctcgtt gcgttcaacg agaagatcgc cgccaaggtg 720
cgccccggct cgttccaggc caagtggctc tcggcgcagg cgtacatttt tgcgccggtg 780
tcctgcttcc tggttggtct cttctggacc ctgtttctgc acccgcgcca catgccgcgc 840
acgagccact ttgctgagat ggccgccgtc gcggtgcgcg tcgtgggctg ggcggcgctc 900
atgcactcgt cgggtacag cgggagcgac tcgttcggtc tctacatggc cacctttggc 960
tttggctgca cctacatctt caccaacttt gcggtcagcc acacgcacct cgacgtcacc 1020
gagccggacg agttcctgca ctgggtcgag tacgccgcgc tgcacacgac caacgtgtcc 1080
aacgactcgt ggttcatcac ctggtggatg tcgtacctca actttcagat cgagcaccac 1140
ctctttccgt cgctgcccca gctcaacgcc ccgcgcgtcg ccccgcgcgt ccgcgccctc 1200
ttcgagaagc acggcatggc ttacgacgag cgcccgtacc ttaccgcgct ggcgacacg 1260
tttgccaacc tgcacgccgt gggccaaaac gcgggccagg cggcggccaa ggccgcttag 1320

<210> 29
<211> 439
<212> PRT
<213> Thraustochytrium aureum

<400> 29
Met Gly Arg Gly Gly Glu Gly Gln Val Asn Ser Ala Gln Val Ala Gln
 1   5   10   15
Gly Gly Ala Gly Thr Arg Lys Thr Ile Leu Ile Glu Gly Glu Val Tyr
            20   25   30
Asp Val Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Phe Leu
        35   40   45
Thr Thr Asp Gly Thr Glu Ala Val Asp Ala Thr Asn Ala Phe Arg Glu
    50   55   60
Phe His Cys Arg Ser Gly Lys Ala Glu Lys Tyr Leu Lys Ser Leu Pro
65   70   75   80
Lys Leu Gly Ala Pro Ser Lys Met Lys Phe Asp Ala Lys Glu Gln Ala
                85   90   95
Arg Arg Asp Ala Ile Thr Arg Asp Tyr Val Lys Leu Arg Glu Glu Met
            100   105   110
Val Ala Glu Gly Leu Phe Lys Pro Ala Pro Leu His Ile Val Tyr Arg
        115   120   125
Phe Ala Glu Ile Ala Ala Leu Phe Ala Ala Ser Phe Tyr Leu Phe Ser
        130   135   140
Met Arg Gly Asn Val Phe Ala Thr Leu Ala Ala Ile Ala Val Gly Gly
145   150   155   160

```
Ile Ala Gln Gly Arg Cys Gly Trp Leu Met His Glu Cys Gly His Phe
              165               170               175
Ser Met Thr Gly Tyr Ile Pro Leu Asp Val Arg Leu Gln Glu Leu Val
              180               185               190
Tyr Gly Val Gly Cys Ser Met Ser Ala Ser Trp Trp Arg Val Gln His
              195               200               205
Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp Leu
      210               215               220
Asp Thr Leu Pro Leu Val Ala Phe Asn Glu Lys Ile Ala Ala Lys Val
225               230               235               240
Arg Pro Gly Ser Phe Gln Ala Lys Trp Leu Ser Ala Gln Ala Tyr Ile
              245               250               255
Phe Ala Pro Val Ser Cys Phe Leu Val Gly Leu Phe Trp Thr Leu Phe
              260               265               270
Leu His Pro Arg His Met Pro Arg Thr Ser His Phe Ala Glu Met Ala
      275               280               285
Ala Val Ala Val Arg Val Val Gly Trp Ala Ala Leu Met His Ser Phe
      290               295               300
Gly Tyr Ser Gly Ser Asp Ser Phe Gly Leu Tyr Met Ala Thr Phe Gly
305               310               315               320
Phe Gly Cys Thr Tyr Ile Phe Thr Asn Phe Ala Val Ser His Thr His
              325               330               335
Leu Asp Val Thr Glu Pro Asp Glu Phe Leu His Trp Val Glu Tyr Ala
              340               345               350
Ala Leu His Thr Thr Asn Val Ser Asn Asp Ser Trp Phe Ile Thr Trp
      355               360               365
Trp Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Ser
370               375               380
Leu Pro Gln Leu Asn Ala Pro Arg Val Ala Pro Arg Val Arg Ala Leu
385               390               395               400
Phe Glu Lys His Gly Met Ala Tyr Asp Glu Arg Pro Tyr Leu Thr Ala
              405               410               415
Leu Gly Asp Thr Phe Ala Asn Leu His Ala Val Gly Gln Asn Ala Gly
              420               425               430
Gln Ala Ala Ala Lys Ala Ala
              435
```

```
<400> 30
gaattcacca tgggtcgcgg agcacaggga gagccaaggc aggccacaga gctgaagagc      60
agcccaagtg agcagcgtaa ggtgttgctc attgacgggc agctgtacga tgcaaccaac     120
ttcaggcatc ctggtggctc catcatcaaa tatttgtgca ccgatggcaa ggaggtagtt     180
gatgcaaccg aagcgtacaa ggagttccac tgcagatcct cgaaggcggt caagtacctc     240
aactccctgc caaagatcga cggcccaatc aagtacaaat acgacgcaaa ggagcaggct     300
cgccatgaca aactcacgag ggagtatgta gctctccgcg aacagctcgt caaggaggga     360
tactttgacc ccagcccgct ccacattatc tacagatgcg ccgagttggc agccatgttc     420
gctctctcgt tctacctttt ctccttcaag ggtaacgtca tggccactat tgctgccatc     480
gtgattgggg ggtgcgtgca gggtcgttgt gggtggctca tgcatgaagc tggccactac     540
agcatgaccg gaaacatccc tgttgacttg cgccttcaag agttttttgta cggaattggg     600
tgtggcatga gcggggcttg gtggagaagc cagcacaaca gcaccacgc cacccccaa      660
aagctcaagc atgacgttga tttggacact cttcctcttg tcgcctggaa cgagaaaatt     720
gcccgtcgcg tcaagccagg tagcttccag gcaaagtggc ttcatctcca gggatacatc     780
```

```
tttgccccag tctcctgcct tctcgttggt ctcttctgga ctttgtactt gcatcctcgc      840
cacatgatcc gcaccaagcg caacttcgag atattttctg tcgctctgcg ctacgtatgc      900
tggttctcgc ttcttttgag catgggctac actgtcggag agtctctggg tctctatgtg      960
cttactttg gacttggctg tacctacatc tttacgcatt ttgctgtaag ccacacccac      1020
ttgccagtgt ccgaggagga cgagtacctg cactgggtcg agtacgctgc gctgcacacc      1080
acgaacgttg ccatcgactc gtacgttgtc acctggctga tgagctacct caactttcag      1140
atcgagcacc acttgttccc ttgctgcccg cagttccgcc accctgcaat ctcttctcgc      1200
gtcaagaaac ttttcgagga caatggtctg gtatacgacg cccgctcata cgtccaggcg      1260
ctcaaggata ccttcggcaa cctacacgaa gtgggcgtca acgctggcca agctgccaag      1320
agcgagtaag atctcgag                                                    1338
```

<210> 31
<211> 439
<212> PRT
<213> Thraustochytrium aureum

<400> 31

```
Met Gly Arg Gly Ala Gln Gly Glu Pro Arg Gln Ala Thr Glu Leu Lys
1               5                   10                  15
Ser Ser Pro Ser Glu Gln Arg Lys Val Leu Leu Ile Asp Gly Gln Leu
            20                  25                  30
Tyr Asp Ala Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Tyr
        35                  40                  45
Leu Cys Thr Asp Gly Lys Glu Val Val Asp Ala Thr Glu Ala Tyr Lys
    50                  55                  60
Glu Phe His Cys Arg Ser Ser Lys Ala Val Lys Tyr Leu Asn Ser Leu
65                  70                  75                  80
Pro Lys Ile Asp Gly Pro Ile Lys Tyr Lys Tyr Asp Ala Lys Glu Gln
                85                  90                  95
Ala Arg His Asp Lys Leu Thr Arg Glu Tyr Val Ala Leu Arg Glu Gln
            100                 105                 110
Leu Val Lys Glu Gly Tyr Phe Asp Pro Ser Pro Leu His Ile Ile Tyr
            115                 120                 125
Arg Cys Ala Glu Leu Ala Ala Met Phe Ala Leu Ser Phe Tyr Leu Phe
    130                 135                 140
Ser Phe Lys Gly Asn Val Met Ala Thr Ile Ala Ala Ile Val Ile Gly
145                 150                 155                 160
Gly Cys Val Gln Gly Arg Cys Gly Trp Leu Met His Glu Ala Gly His
                165                 170                 175
Tyr Ser Met Thr Gly Asn Ile Pro Val Asp Leu Arg Leu Gln Glu Phe
            180                 185                 190
Leu Tyr Gly Ile Gly Cys Gly Met Ser Gly Ala Trp Trp Arg Ser Gln
            195                 200                 205
His Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp
    210                 215                 220
Leu Asp Thr Leu Pro Leu Val Ala Trp Asn Glu Lys Ile Ala Arg Arg
225                 230                 235                 240
Val Lys Pro Gly Ser Phe Gln Ala Lys Trp Leu His Leu Gln Gly Tyr
                245                 250                 255
Ile Phe Ala Pro Val Ser Cys Leu Leu Val Gly Leu Phe Trp Thr Leu
            260                 265                 270
Tyr Leu His Pro Arg His Met Ile Arg Thr Lys Arg Asn Phe Glu Ile
    275                 280                 285
Phe Ser Val Ala Leu Arg Tyr Val Cys Trp Phe Ser Leu Leu Leu Ser
    290                 295                 300
Met Gly Tyr Thr Val Gly Glu Ser Leu Gly Leu Tyr Val Leu Thr Phe
305                 310                 315                 320
```

```
Gly Leu Gly Cys Thr Tyr Ile Phe Thr His Phe Ala Val Ser His Thr
              325                 330                 335
His Leu Pro Val Ser Glu Glu Asp Glu Tyr Leu His Trp Val Glu Tyr
              340                 345                 350
Ala Ala Leu His Thr Thr Asn Val Ala Ile Asp Ser Tyr Val Val Thr
              355                 360                 365
Trp Leu Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro
      370                 375                 380
Cys Cys Pro Gln Phe Arg His Pro Ala Ile Ser Ser Arg Val Lys Lys
385                 390                 395                 400
Leu Phe Glu Asp Asn Gly Leu Val Tyr Asp Ala Arg Ser Tyr Val Gln
                  405                 410                 415
Ala Leu Lys Asp Thr Phe Gly Asn Leu His Glu Val Gly Val Asn Ala
                  420                 425                 430
Gly Gln Ala Ala Lys Ser Glu
              435
```

```
<210> 32
<211> 1381
<212> DNA
<213> Thraustochytrium aureum

<400> 32
ccatgggccg cggcggcgag aaaagcgagg tggaccaggt gcagccacaa aagaccgagc      60
agctccagaa ggccaagtgg gaggatgttg ttcgcatcaa tggagtcgaa tacgacgtca     120
cggactatct cagaaaacac cctggtggca gcgtgatcaa gtacgggctt gccaacaccg     180
gcgctgatgc cacgtccctc tttgaagcgt tccacatgcg ctcaaagaag gctcagatgg     240
tgctcaagtc tctcccaaag cgtgctccgg tcctcgagat ccagccaaac cagcttccag     300
aggagcagac caaggaggcg gagatgctgc gtgattttaa aaaatttgag gatgagattc     360
gccgggatgg attgatggaa ccttccttct ggcatcgcgc ttacagatta tcagagcttg     420
taggtatgtt cacgctcggc ctctacctct tctcgttaaa cactcctctg tctattgctg     480
ctggtgtcct cgtccacggt ctctttggtg cattctgtgg atggtgccag catgaggcag     540
gccacggctc ctttttttac agcctttggt ggggcaagcg tgtacaggcc atgttgatcg     600
ggtttggtct aggaacatcc ggcgacatgt ggaacatgat gcacaacaag catcatgctg     660
ccacccaaaa ggttcatcac gaccttgaca ttgacacaac tccttttgta gctttcttca     720
acactgcatt tgagaaaaac agatggaagg ctttttccaa ggcttgggtc cgctttcagg     780
ctttcacgtt cattcctgtc accagcggca tgatcgtcat gctgttctgg ctgtttttc      840
tccaccctcg ccgcgtcgtt caaaagaaga actttgagga gggtttttgg atgctgtcga     900
gccacattgt gcgcacctat ctcttccacc ttgtgaccgg ctgggagagc ctcgctgcat     960
gctaccttgt tgggtattgg gcgtgcatgt gggtgtccgg tatgtatttg tttggccact    1020
tttcgctctc ccacactcat atggacattg tggaggcgga cgtgcataag aactgggtca    1080
ggtacgctgt tgaccacact gttgacatca gcccatccaa cccgctcgtg tgctgggtca    1140
tgggttacct caacatgcag accatccacc acttgtggcc tgccatgccc cagtaccacc    1200
aggtcgaggt ctcacgccgc tttgccatct cgccaaaaaa cacggcctc aactaccgcg     1260
tcgtctctta ctttgaggct tggcgcctga tgctccaaaa tcttgctgac gtcggttccc    1320
actaccatga gaacggtgtc aagcgcgccc caaagaaagc caaggcgcag tagaaagcta    1380
t                                                                     1381
```

```
<210> 33
<211> 456
<212> PRT
<213> Thraustochytrium aureum

<400> 33
Met Gly Arg Gly Gly Glu Lys Ser Glu Val Asp Gln Val Gln Pro Gln
  1               5                  10                  15
Lys Thr Glu Gln Leu Gln Lys Ala Lys Trp Glu Asp Val Val Arg Ile
```

```
                     20                        25                        30
    Asn Gly Val Glu Tyr Asp Val Thr Asp Tyr Leu Arg Lys His Pro Gly
                     35                        40                        45
    Gly Ser Val Ile Lys Tyr Gly Leu Ala Asn Thr Gly Ala Asp Ala Thr
                     50                        55                        60
    Ser Leu Phe Glu Ala Phe His Met Arg Ser Lys Lys Ala Gln Met Val
    65                        70                        75                        80
    Leu Lys Ser Leu Pro Lys Arg Ala Pro Val Leu Glu Ile Gln Pro Asn
                     85                        90                        95
    Gln Leu Pro Glu Glu Gln Thr Lys Glu Ala Glu Met Leu Arg Asp Phe
                     100                       105                       110
    Lys Lys Phe Glu Asp Glu Ile Arg Arg Asp Gly Leu Met Glu Pro Ser
                     115                       120                       125
    Phe Trp His Arg Ala Tyr Arg Leu Ser Glu Leu Val Gly Met Phe Thr
                     130                       135                       140
    Leu Gly Leu Tyr Leu Phe Ser Leu Asn Thr Pro Leu Ser Ile Ala Ala
    145                       150                       155                       160
    Gly Val Leu Val His Gly Leu Phe Gly Ala Phe Cys Gly Trp Cys Gln
                     165                       170                       175
    His Glu Ala Gly His Gly Ser Phe Phe Tyr Ser Leu Trp Trp Gly Lys
                     180                       185                       190
    Arg Val Gln Ala Met Leu Ile Gly Phe Gly Leu Gly Thr Ser Gly Asp
                     195                       200                       205
    Met Trp Asn Met Met His Asn Lys His His Ala Ala Thr Gln Lys Val
    210                       215                       220
    His His Asp Leu Asp Ile Asp Thr Thr Pro Phe Val Ala Phe Phe Asn
    225                       230                       235                       240
    Thr Ala Phe Glu Lys Asn Arg Trp Lys Gly Phe Ser Lys Ala Trp Val
                     245                       250                       255
    Arg Phe Gln Ala Phe Thr Phe Ile Pro Val Thr Ser Gly Met Ile Val
                     260                       265                       270
    Met Leu Phe Trp Leu Phe Phe Leu His Pro Arg Arg Val Val Gln Lys
                     275                       280                       285
    Lys Asn Phe Glu Glu Gly Phe Trp Met Leu Ser Ser His Ile Val Arg
                     290                       295                       300
    Thr Tyr Leu Phe His Leu Val Thr Gly Trp Glu Ser Leu Ala Ala Cys
    305                       310                       315                       320
    Tyr Leu Val Gly Tyr Trp Ala Cys Met Trp Val Ser Gly Met Tyr Leu
                     325                       330                       335
    Phe Gly His Phe Ser Leu Ser His Thr His Met Asp Ile Val Glu Ala
                     340                       345                       350
    Asp Val His Lys Asn Trp Val Arg Tyr Ala Val Asp His Thr Val Asp
                     355                       360                       365
    Ile Ser Pro Ser Asn Pro Leu Val Cys Trp Val Met Gly Tyr Leu Asn
                     370                       375                       380
    Met Gln Thr Ile His His Leu Trp Pro Ala Met Pro Gln Tyr His Gln
    385                       390                       395                       400
    Val Glu Val Ser Arg Arg Phe Ala Ile Phe Ala Lys Lys His Gly Leu
                     405                       410                       415
    Asn Tyr Arg Val Val Ser Tyr Phe Glu Ala Trp Arg Leu Met Leu Gln
                     420                       425                       430
    Asn Leu Ala Asp Val Gly Ser His Tyr His Glu Asn Gly Val Lys Arg
                     435                       440                       445
    Ala Pro Lys Lys Ala Lys Ala Gln
    450                       455
```

<210> 34

<210> 1329
<212> DNA
<213> Isochrysis galbana

<400> 34
```
atggtggcag gcaaatcagg cgctgcggcg cacgtgactc acagctcgac attgccccgt      60
gagtaccatg gcgcgaccaa cgactcgcgc tctgaggcgg ccgacgtcac cgtctctagc     120
atcgatgctg aaaaggagat gatcatcaac ggccgcgtgt atgacgtgtc gtcatttgtg     180
aagcggcacc caggtggctc ggtgatcaag ttccagctgg gcgccgacgc gagcgacgcg     240
tacaacaact ttcacgtccg ctccaagaag gcggacaaga tgctgtattc gctcccgtcc     300
cggccggccg aggccggcta cgcccaggac gacatctccc gcgactttga gaagctgcgc     360
ctcgagctga aggaggaggg ctacttcgag cccaacctgg tgcacgtgag ctacaggtgt     420
gtggaggttc ttgccatgta ctgggctggc gtccagctca tctggtccgg gtactggttc     480
ctcggcgcga tcgtggccgg cattgcgcag ggccgctgcg gctggctcca gcatgagggt     540
gggcactact cgctcaccgg caacatcaag atcgaccggc atctgcagat ggccatctat     600
gggcttggct gcggcatgtc gggctgctac tggcgcaacc agcacaacaa gcaccacgcc     660
acgccgcaga agctcgggac cgaccccgac ctgcagacga tgccgctggt ggccttccac     720
aagatcgtcg cgccaaggc gcgaggcaag ggcaaggcgt ggctggcgtg gcaggcgccg     780
ctcttctttg gcgggatcat ctgctcgctc gtctctttcg gctggcagtt cgtgctccac     840
cccaaccacg cgctgcgcgt gcacaatcac ctggagctcg cgtacatggg cctgcggtac     900
gtgctgtggc acctggcctt tggccacctc gggctgctga gctcgctccg cctgtacgcc     960
ttttacgtgg ccgtgggcgg cacctacatc ttcaccaact tcgccgtctc gcacacccac    1020
aaggacgtcg tcccgcccac caagcacatc tcgtgggcac tctactcggc caaccacacg    1080
accaactgct ccgactcgcc ctttgtcaac tggtggatgg cctacctcaa cttccagatc    1140
gagcaccacc tcttcccgtc gatgccgcag tacaaccacc caagatcgc cccgcgggtg    1200
cgcgcgctct cgagaagca cggggtcgag tatgacgtcc ggccatacct ggagtgtttt    1260
cgggtcacgt acgtcaacct gctcgccgta ggcaacccgg agcactccta ccacgagcac    1320
acgcactag                                                            1329
```

<210> 35
<211> 442
<212> PRT
<213> Isochrysis galbana

<400> 35
```
Met Val Ala Gly Lys Ser Gly Ala Ala Ala His Val Thr His Ser Ser
1               5                   10                  15
Thr Leu Pro Arg Glu Tyr His Gly Ala Thr Asn Asp Ser Arg Ser Glu
            20                  25                  30
Ala Ala Asp Val Thr Val Ser Ser Ile Asp Ala Glu Lys Glu Met Ile
        35                  40                  45
Ile Asn Gly Arg Val Tyr Asp Val Ser Ser Phe Val Lys Arg His Pro
    50                  55                  60
Gly Gly Ser Val Ile Lys Phe Gln Leu Gly Ala Asp Ala Ser Asp Ala
65                  70                  75                  80
Tyr Asn Asn Phe His Val Arg Ser Lys Lys Ala Asp Lys Met Leu Tyr
                85                  90                  95
Ser Leu Pro Ser Arg Pro Ala Glu Ala Gly Tyr Ala Gln Asp Asp Ile
            100                 105                 110
Ser Arg Asp Phe Glu Lys Leu Arg Leu Glu Leu Lys Glu Glu Gly Tyr
        115                 120                 125
Phe Glu Pro Asn Leu Val His Val Ser Tyr Arg Cys Val Glu Val Leu
    130                 135                 140
Ala Met Tyr Trp Ala Gly Val Gln Leu Ile Trp Ser Gly Tyr Trp Phe
145                 150                 155                 160
Leu Gly Ala Ile Val Ala Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu
                165                 170                 175
```

```
Gln His Glu Gly Gly His Tyr Ser Leu Thr Gly Asn Ile Lys Ile Asp
            180                 185                 190
Arg His Leu Gln Met Ala Ile Tyr Gly Leu Gly Cys Gly Met Ser Gly
        195                 200                 205
Cys Tyr Trp Arg Asn Gln His Asn Lys His His Ala Thr Pro Gln Lys
    210                 215                 220
Leu Gly Thr Asp Pro Asp Leu Gln Thr Met Pro Leu Val Ala Phe His
225                 230                 235                 240
Lys Ile Val Gly Ala Lys Ala Arg Gly Lys Gly Lys Ala Trp Leu Ala
                245                 250                 255
Trp Gln Ala Pro Leu Phe Phe Gly Gly Ile Ile Cys Ser Leu Val Ser
                260                 265                 270
Phe Gly Trp Gln Phe Val Leu His Pro Asn His Ala Leu Arg Val His
        275                 280                 285
Asn His Leu Glu Leu Ala Tyr Met Gly Leu Arg Tyr Val Leu Trp His
        290                 295                 300
Leu Ala Phe Gly His Leu Gly Leu Leu Ser Ser Leu Arg Leu Tyr Ala
305                 310                 315                 320
Phe Tyr Val Ala Val Gly Gly Thr Tyr Ile Phe Thr Asn Phe Ala Val
                325                 330                 335
Ser His Thr His Lys Asp Val Val Pro Pro Thr Lys His Ile Ser Trp
            340                 345                 350
Ala Leu Tyr Ser Ala Asn His Thr Thr Asn Cys Ser Asp Ser Pro Phe
            355                 360                 365
Val Asn Trp Trp Met Ala Tyr Leu Asn Phe Gln Ile Glu His His Leu
    370                 375                 380
Phe Pro Ser Met Pro Gln Tyr Asn His Pro Lys Ile Ala Pro Arg Val
385                 390                 395                 400
Arg Ala Leu Phe Glu Lys His Gly Val Glu Tyr Asp Val Arg Pro Tyr
                405                 410                 415
Leu Glu Cys Phe Arg Val Thr Tyr Val Asn Leu Leu Ala Val Gly Asn
            420                 425                 430
Pro Glu His Ser Tyr His Glu His Thr His
            435                 440
```

<210> 36
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO838

<221> misc_feature
<222> (7)...(7)
<223> v = a or g or c at position 7

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (13)...(13)
<223> s = g or c at position 13

<221> misc_feature
<222> (16)...(16)

<223> r = g or a at position 16

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (22)...(22)
<223> y = t/u or c at position 22

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
<223> r = g or a at position 31

<400> 36
catggtvggr aasagrtgrt gytcratctg rtagtt   36

<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1065

<400> 37
cgacaagagg aagagtgtcc aaatc   25

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1064

<400> 38
cgccttcaag agttttttgta cggaattggg   30

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1097

<400> 39
cttgtaccat gggtcgcgga gcacagggag   30

<210> 40
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer RO1098

<400> 40
tgaagcttac tcgctcttgg cagcttggcc   30

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1107

<400> 41
tttaaccatg ggccgcggcg gcgagaaaag   30

<210> 42
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1108

<400> 42
gggaagaagc tttctactgc gccttggctt tctttg   36

<210> 43
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1235

<400> 43
cgaagttggt gaagatgtag gtgccg   26

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1232

<400> 44
gagcgacgcg tacaacaact ttcacgt   27

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
cgactggagc acgaggacac tga   23

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> GeneRacer 3 Prime Primer

<400> 46
gctgtcaacg atacgctacg taacg   25

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Nested Primer RO1234

<400> 47
agctccaggt gattgtgcac gcgcag   26

<210> 48
<211> 27
<212> DNA
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 1   5   10

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<212> PRT
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<220>
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<400> 55
Asn Tyr Gln Ile Glu His His Leu Phe Pro Thr Met
 1   5   10